



IFW16

## RAW SEQUENCE LISTING

DATE: 08/11/2004

PATENT APPLICATION: US/10/088,467

TIME: 16:14:14

Input Set : A:\FCCC- US- Tew (ABCA2) Sequence Listing.txt

Output Set: N:\CRF4\08112004\J088467.raw

4 <110> APPLICANT: Tew, Kenneth D.  
5 Vulevic, Bojana  
6 Chen, Zhijian  
8 <120> TITLE OF INVENTION: Nucleic Acid Encoding Human ABCA  
9 Transporter 2 and Methods of Use Thereof  
11 <130> FILE REFERENCE: FCCC.99-08US  
13 <140> CURRENT APPLICATION NUMBER: 10/088,467  
14 <141> CURRENT FILING DATE: 2002-06-24  
16 <150> PRIOR APPLICATION NUMBER: PCT/US00/40789  
17 <151> PRIOR FILING DATE: 2000-08-31  
19 <150> PRIOR APPLICATION NUMBER: 60/154,839  
20 <151> PRIOR FILING DATE: 1999-09-20  
22 <160> NUMBER OF SEQ ID NOS: 36  
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 8040  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Homo sapiens  
32 <400> SEQUENCE: 1

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34 gctgctctgg aagaacgtga cgctcaaacy cggagcccg tgggtcctgg ccttcgagat 120  
35 cttcatcccc ctggtgctgt tctttatcct gctggggctg cgacagaaga agcccaccat 180  
36 ctccgtgaag gaagtcccc tctacacagc ggcgccccctg acgtctgccc gcatcctgcc 240  
37 tgtcatgcaa tegtctgccc cggacggcca cgcagacgag ttcggtctcc tgcagtacgc 300  
38 caactccacg gtcacgcagc gcttgagcgt cctggaccgc gtgggtggagg aaggcaacct 360  
39 gtttgaccca gcgcggccca gcctgggctc agagctcgag gccctacgcc agcatctgga 420  
40 ggcctcagtg ggcggcccg gcaactcggg gagccacctg gacagatcca cagtgtcttc 480  
41 cttctctctg gactcggtgg ccagaaaccc gcaggagctc tggcgtttcc tgacgcaaaa 540  
42 cttgtcgtcg cccaatagca cggcccaagc actcttgccc gcccggtgtg acccgccga 600  
43 ggtctaccac ctgctctttg gtccctcatc tgccctggat tcacagtctg gctccacaa 660  
44 gggtcaggag ccttgaggcc gcctaggggg caatcccttg ttccggatgg aggagctgct 720  
45 gctggctcct gccctcctgg agcagctcac ctgcacgccc ggctcggggg agctgggccc 780  
46 gatcctcact gtgcctgaga gtcagaaggg agccctgcag ggctaccggg atgctgtctg 840  
47 cagtgggcag gctgctgcgc gtgccaggcg cttctctggg ctgtctgctg agctccggaa 900  
48 ccagctggac gtggccaagg tctcccagca gctgggcttg gatgccccca acggctcgga 960  
49 ctccctcgca caggcgccac ccccacggag gctgcaggcg cttctggggg acctgctgga 1020  
50 tgcccagaag gttctgcagg atgtggatgt cctgtcgccc ctggccctgc tactgcccc 1080  
51 ggggtgcctgc actggccgga ccccggacc ccagccagt ggtgcgggtg gggcgccaa 1140  
52 tggcactggg gcaggggcag tcatgggccc caacgccacc gctgaggagg gcgcaccctc 1200  
53 tgctgcagca ctggccaccc cggacacgct gcaggggcag tgctcagcct tegtacagct 1260  
54 ctggggccggc ctgcagccca ctttgtgtgg caacaaccgc accattgaac ccgaggcgct 1320  
55 gcggcgggggc aactgagct ccctgggctt cactgagcaag gagcagcgga acctgggctt 1380  
56 cctcgtgcac ctcatgacca gcaaccccaa aatcctgtac gcgcctgcgg gctctgaggt 1440



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57	cgaccgcgtc	atcctcaagg	ccaacgagac	ttttgctttt	gtgggcaacg	tgactcacta	1500
58	tgcccaggtc	tggtcaca	tctcgcgga	gatccgcagc	ttcctggagc	agggcaggct	1560
59	gcagcaacac	ctgcgctggc	tgacgcagta	tgtagcagag	ctgcggtgc	accccagggc	1620
60	actgaacctg	tactggatg	agctgccgcc	ggccctgaga	caggacaact	tctcgctgcc	1680
61	cagtggcatg	gccctctgc	agcagctgga	taccattgac	aacgcggcct	gcggctggat	1740
62	ccagttcatg	tccaaggtga	gcgtggacat	cttcaagggc	ttccccgacg	aggagagcat	1800
63	tgtcaactac	accctcaacc	aggcctacca	ggacaacgtc	actgtttttg	ccagtgtgat	1860
64	cttccagacc	cggaaggacg	gctcgctccc	gcctcacgtg	cactacaaga	tccgccagaa	1920
65	ctccagcttc	accgagaaaa	ccaacgagat	ccgcgcgcgc	tactggcggc	ctgggccc aa	1980
66	tactggcggc	cgcttctact	tcctctacgg	cttcgtctgg	atccaggaca	tgatggagcg	2040
67	cgccatcatc	gacacttttg	tggggcacga	cggtgtggag	ccaggcagct	acgtgcagat	2100
68	gttcccctac	ccctgctaca	cacgcgatga	cttctgttt	gtcattgagc	acatgatgcc	2160
69	gctgtgcatg	gtgatctcct	gggtctactc	cgtggccatg	accatccagc	acatcgtggc	2220
70	ggagaaggag	caccggctca	aggaggtgat	gaagaccatg	ggcctgaaca	acgcggtgca	2280
71	ctgggtggcc	tggttcatca	ccggctttgt	gcagctgtcc	atctccgtga	cagcactcac	2340
72	cgccatcctg	aagtacggcc	aggtgcttat	gcacagccac	gtgggtcatca	tctggctctt	2400
73	cctggcagtc	tacgcggtgg	ccaccatcat	gttctgcttc	ctgggtgtctg	tgctgtactc	2460
74	caaggccaag	ctggcctcgg	cctgcggtgg	catcatctac	ttcctgagct	acgtgcccta	2520
75	catgtacgtg	gcgatccgag	aggaggtggc	gcataataag	atcacggcct	tcgagaagtg	2580
76	catcgctcc	ctcatgtcca	cgacggcctt	tgggtctggc	tctaagtact	tcgcgctgta	2640
77	tgaggtggcc	ggcgtgggca	tccagtggca	caccttcagc	cagtcccccg	tggaggggga	2700
78	cgacttcaac	ttgctcctgg	ctgtcaccat	gctgatgggtg	gacgcctgtg	tctatggcat	2760
79	cctcacgtgg	tacattgagg	ctgtgcaccc	aggcatgtac	gggctgcccc	ggccctggta	2820
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82	ggagagccgg	cgctttgagg	agaccctgtg	catggaggag	gagcccaccc	acctgcctct	3000
83	ggttgtctgc	gtggacaaac	tcaccaaggt	ctacaaggac	gacaagaagc	tggccctgaa	3060
84	caagctgagc	ctgaacctct	acgagaacca	ggtggtctcc	ttcttggggc	acaacggggc	3120
85	gggcaagacc	accaccatgt	ccatcctgac	cggcctgttc	cctccaacgt	cgggttccgc	3180
86	caccactctac	gggcacgaca	tccgcacgga	gatggatgag	atccgcaaga	acctgggcac	3240
87	gtgcccgcag	cacaatgtgc	tctttgaccg	gctcacgggtg	gaggaaacacc	tctggttcta	3300
88	ctcacggctc	aagagcatgg	ctcaggagga	gatccgcaga	gagatggaca	agatgatcga	3360
89	ggacctggag	ctctccaaca	aacggcactc	actggtgcag	acattgtcgg	gtggcatgaa	3420
90	gcgcaagctg	tccgtggcca	tcgccttcgt	gggcggctct	cgcgccatca	tcctggacga	3480
91	gcccacggcg	ggcgtggacc	cctacgcgcg	ccgcgccatc	tgggacctca	tcctgaagta	3540
92	caagccaggc	cgcaccatcc	ttctgtccac	ccaccacatg	gatgaggctg	acctgcttgg	3600
93	ggaccgcatt	gccatcatct	cccatgggaa	gctcaagtgc	tgcggctccc	cgtcttctct	3660
94	caagggcacc	tatggcgacg	ggtaccgcct	cacgtgggtc	aagcggcccg	ccgagccggg	3720
95	gggcccccaa	gagccagggc	tggcatccag	ccccccagg	cgggccccgc	tgagcagctg	3780
96	ctccgagctc	caggtgtccc	agttcatccg	caagcatgtg	gcctcctgcc	tgctggtctc	3840
97	agacacaagc	acggagctct	cctacatcct	gcccagcgag	gccgccaaga	agggggcttt	3900
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99	gctgatggac	acgacctgg	aggaagtgtt	cctcaagggtg	tggaggagg	atcagtcgct	4020
100	ggagaacagt	gaggccgatg	tgaaggagtc	caggaaggat	gtgctccctg	gggcggaggg	4080
101	cccggcgtct	ggggagggtc	acgctggcaa	tctggcccg	tgctcggagc	tgaccagtc	4140
102	gcaggcatcg	ctgcagtcgg	cgatcatctgt	gggctctgcc	cgtggcgacg	agggagctgg	4200
103	ctacaccgac	gtctatggcg	actaccgccc	cctctttgat	aaccacagg	accagacaa	4260
104	tgtcagcctg	caagaggtgg	aggcagaggc	cctgtcgagg	gtcggccagg	gcagccgcaa	4320
105	gctggacggc	gggtggctga	aggtgcgcca	gttccacggg	ctgctggtca	aacgcttcca	4380

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106	ctgcgcccgc	cgcaactcca	aggcactctt	ctcccagatc	ttgctgccag	ccttcttcgt	4440
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108	cctgtcacct	tcccagtacc	acaactacac	ccagccccgt	ggcaatttca	tcccctacgc	4560
109	caacgaggag	cgccgcgagt	accggtcgcg	gctatcgccc	gacgccagcc	cccagcagct	4620
110	cgtgagcacg	ttccggctgc	cgtcgggggt	gggtgccacc	tgcgtgctca	agtctccgcg	4680
111	caacggctcg	ctggggccca	cgttgaacct	gagcagcggg	gagtcgcgcc	tgctggcggc	4740
112	tcggtttctt	gacagcatgt	gtctggagtc	cttcacacag	gggctgccac	tgtccaattt	4800
113	cgtgccaccc	ccaccctcgc	ccgccccatc	tgactcgcca	gcgtccccgg	atgaggacct	4860
114	gcaggcctgg	aacgtctccc	tgccgcccac	cgctgggcca	gaaatgtgga	cgtcggcacc	4920
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117	catectgacc	gacatcaccc	gccacaatgt	ctctgagtac	ctgctcttca	cctccgaccg	5100
118	cttccgactg	caccggatat	gggccatcac	ctttggaaac	gtcctgaagt	ccatcccagc	5160
119	ctcatttggc	accaggggcc	caccatgggt	gcggaagatc	gcggtgccga	gggctgcccc	5220
120	ggttttctac	aacaacaagg	gctatcacag	catgcccacc	tacctcaaca	gcctcaacaa	5280
121	cgccatcctg	cgtgcacaac	tgcccaagag	caagggcaac	ccggcggttt	acggcatcac	5340
122	cgtcaccaac	caccccatga	ataagaccag	cgccagcctc	tccctggatt	acctgctgca	5400
123	gggcacggat	gtcgtcatcg	ccatcttcat	catcgtggcc	atgtccttcg	tgccggccag	5460
124	cttcgttgtc	ttcctcgtgg	ccgagaagtc	caccaaggcc	aagcatctgc	agtttgctag	5520
125	cggctgcaac	cccatcatct	actggctggc	gaactacgtg	tgggacatgc	tcaactacct	5580
126	ggtccccgct	acctgctgtg	tcatcatcct	gtttgtgttc	gacctgccgg	cctacacgtc	5640
127	gcccaccaac	ttccttgccg	tctctccct	cttctcgttc	tatgggtggg	ccatcacgcc	5700
128	catcatgtac	ccggcctcct	tctggttcga	ggtccccagc	tccgcctacg	tgttcctcat	5760
129	tgctcatcaat	ctcttcatcg	gcataccgcg	caccgtggcc	accttcctgc	tacagctctt	5820
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136	catgggtcaag	attgagaacc	tgaccaagggt	ctacaagtcc	cggaagattg	gccgtatcct	6240
137	ggcgttgac	cgcctgtgcc	tgggtgtgcg	tctggcgag	tgcttcgggc	tctggggcgt	6300
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146	cgaggcgtg	tgacgcggc	tggccatcat	ggtgaacggg	cgcctgcggg	gcctgggcag	6840
147	catccagcac	ctgaagaacc	ggtttggaga	tggtacatg	atcacggtgc	ggaccaagag	6900
148	cagccagagt	gtgaaggacg	tgggtgcggt	cttcaaccgc	aacttcccgg	aagccatgct	6960
149	caaggagcgg	caccacacaa	aggtgcagta	ccagctcaag	tggagcaca	tctcgtggc	7020
150	ccaggtgttc	agcaagatgg	agcaggtgtc	tggcgtgctg	ggcatcgagg	actactcggg	7080
151	cagccagacc	acactggaca	atgtgttcgt	gaactttgcc	aagaagcaga	gtgacaacct	7140
152	ggagcagcag	gagacggagc	cgcctccgc	actcagtc	cctctcggct	gcttgctcag	7200
153	cctgctccgg	ccccggtctg	cccccaacga	gctccgggca	cttggtgcag	acgagcccga	7260
154	ggacctggac	acggaggacg	agggcctcat	cagcttcgag	gaggagcggg	cccagctgtc	7320

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155 cttcaacacg gacacgctct gctgaccacc cagagctggg ccagggagga cacgctccac 7380
156 tgaccaccca gagctgggcc agggactcaa caatggggac agaagtcccc cagtgcctgc 7440
157 cagggcctgg agtggaggtt caggaccaag gggcttctgg tctccagcc cctgtactcg 7500
158 gccatgccct gcggtcactg cggttgccgc ccctaattgt gccaaaggct gacccggccc 7560
159 gggctgcgta cacccttgcc ctgctttgcc ttaaagcctc ggggtctgcc cgccccctcg 7620
160 cccctgcctg gcactgctca ccgccaagg cgacgccggc tggaccaggc actgctggcc 7680
161 tttctcctgc ccggcctcgg aaccagcttt tctctcttac gatgaaggct gatgccgaga 7740
162 gcgggctgtg ggcgagctg ggtcagtcct gtatttatct tgctttgaga agaggctcct 7800
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164 ctggcaggtg gcaggaatgg agaagctgac cctgctggcc aggcaagggg ccagaccccc 7920
165 cccaaccccc agctgccatc gctctccac ccagcttggc cccctgcccg cccacctccc 7980
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169 <210> SEQ ID NO: 2
170 <211> LENGTH: 2436
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 2
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178 20 25 30
179 Leu Val Leu Phe Phe Ile Leu Leu Gly Leu Arg Gln Lys Lys Pro Thr
180 35 40 45
181 Ile Ser Val Lys Glu Val Pro Phe Tyr Thr Ala Ala Pro Leu Thr Ser
182 50 55 60
183 Ala Gly Ile Leu Pro Val Met Gln Ser Leu Cys Pro Asp Gly Gln Arg
184 65 70 75 80
185 Asp Glu Phe Gly Phe Leu Gln Tyr Ala Asn Ser Thr Val Thr Gln Leu
186 85 90 95
187 Leu Glu Arg Leu Asp Arg Val Val Glu Gly Asn Leu Phe Asp Pro
188 100 105 110
189 Ala Arg Pro Ser Leu Gly Ser Glu Leu Glu Ala Leu Arg Gln His Leu
190 115 120 125
191 Glu Ala Leu Ser Ala Gly Pro Gly Thr Ser Gly Ser His Leu Asp Arg
192 130 135 140
193 Ser Thr Val Ser Ser Phe Ser Leu Asp Ser Val Ala Arg Asn Pro Gln
194 145 150 155 160
195 Glu Leu Trp Arg Phe Leu Thr Gln Asn Leu Ser Leu Pro Asn Ser Thr
196 165 170 175
197 Ala Gln Ala Leu Leu Ala Ala Arg Val Asp Pro Pro Glu Val Tyr His
198 180 185 190
199 Leu Leu Phe Gly Pro Ser Ser Ala Leu Asp Ser Gln Ser Gly Leu His
200 195 200 205
201 Lys Gly Gln Glu Pro Trp Ser Arg Leu Gly Gly Asn Pro Leu Phe Arg
202 210 215 220
203 Met Glu Glu Leu Leu Leu Ala Pro Ala Leu Leu Glu Gln Leu Thr Cys
204 225 230 235 240
205 Thr Pro Gly Ser Gly Glu Leu Gly Arg Ile Leu Thr Val Pro Glu Ser
206 245 250 255

```

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```

207 Gln Lys Gly Ala Leu Gln Gly Tyr Arg Asp Ala Val Cys Ser Gly Gln
208                260                265                270
209 Ala Ala Ala Arg Ala Arg Arg Phe Ser Gly Leu Ser Ala Glu Leu Arg
210                275                280                285
211 Asn Gln Leu Asp Val Ala Lys Val Ser Gln Gln Leu Gly Leu Asp Ala
212                290                295                300
213 Pro Asn Gly Ser Asp Ser Ser Pro Gln Ala Pro Pro Pro Arg Arg Leu
214                305                310                315                320
215 Gln Ala Leu Leu Gly Asp Leu Leu Asp Ala Gln Lys Val Leu Gln Asp
216                325                330                335
217 Val Asp Val Leu Ser Ala Leu Ala Leu Leu Leu Pro Gln Gly Ala Cys
218                340                345                350
219 Thr Gly Arg Thr Pro Gly Pro Pro Ala Ser Gly Ala Gly Gly Ala Ala
220                355                360                365
221 Asn Gly Thr Gly Ala Gly Ala Val Met Gly Pro Asn Ala Thr Ala Glu
222                370                375                380
223 Glu Gly Ala Pro Ser Ala Ala Ala Leu Ala Thr Pro Asp Thr Leu Gln
224                385                390                395                400
225 Gly Gln Cys Ser Ala Phe Val Gln Leu Trp Ala Gly Leu Gln Pro Ile
226                405                410                415
227 Leu Cys Gly Asn Asn Arg Thr Ile Glu Pro Glu Ala Leu Arg Arg Gly
228                420                425                430
229 Asn Met Ser Ser Leu Gly Phe Thr Ser Lys Glu Gln Arg Asn Leu Gly
230                435                440                445
231 Leu Leu Val His Leu Met Thr Ser Asn Pro Lys Ile Leu Tyr Ala Pro
232                450                455                460
233 Ala Gly Ser Glu Val Asp Arg Val Ile Leu Lys Ala Asn Glu Thr Phe
234                465                470                475                480
235 Ala Phe Val Gly Asn Val Thr His Tyr Ala Gln Val Trp Leu Asn Ile
236                485                490                495
237 Ser Ala Glu Ile Arg Ser Phe Leu Glu Gln Gly Arg Leu Gln Gln His
238                500                505                510
239 Leu Arg Trp Leu Gln Gln Tyr Val Ala Glu Leu Arg Leu His Pro Glu
240                515                520                525
241 Ala Leu Asn Leu Ser Leu Asp Glu Leu Pro Pro Ala Leu Arg Gln Asp
242                530                535                540
243 Asn Phe Ser Leu Pro Ser Gly Met Ala Leu Leu Gln Gln Leu Asp Thr
244                545                550                555                560
245 Ile Asp Asn Ala Ala Cys Gly Trp Ile Gln Phe Met Ser Lys Val Ser
246                565                570                575
247 Val Asp Ile Phe Lys Gly Phe Pro Asp Glu Glu Ser Ile Val Asn Tyr
248                580                585                590
249 Thr Leu Asn Gln Ala Tyr Gln Asp Asn Val Thr Val Phe Ala Ser Val
250                595                600                605
251 Ile Phe Gln Thr Arg Lys Asp Gly Ser Leu Pro Pro His Val His Tyr
252                610                615                620
253 Lys Ile Arg Gln Asn Ser Ser Phe Thr Glu Lys Thr Asn Glu Ile Arg
254                625                630                635                640
255 Arg Ala Tyr Trp Arg Pro Gly Pro Asn Thr Gly Gly Arg Phe Tyr Phe

```

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:20; N Pos. 24,25,29,30,34,35

**VERIFICATION SUMMARY**

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L:698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0